

GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 14, 2003, 03:05:54 ; Search time 4433 Seconds  
(without alignments)  
3932.457 Million cell updates/sec

Title: US-09-846-589A-10  
Perfect score: 599  
Sequence: 1 TLPCLLSTTPLSPPPPPQI.....MDEPSGTVWRPCEPERSEES 599

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4106490

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool/US09846589/runat\_13012003\_094912\_7742/app\_query.fasta\_1.77  
5

-DB=GenEmbl -QFMT=fastap -SUFFIX=olip2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=quality -THR\_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto  
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09846589\_@CGN\_1\_1\_1879\_@runat\_13012003\_094912\_7742 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*

Seq Search Summary  
for Seq 10  
(amino acid against DNA)  
Oligo

\* missing search in Issued Patents  
but sufficient overlap w/other searches ✓ OK

```

11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	599	100.0	2085	6	AR160636	AR160636 Sequence
2	76	12.7	1957	6	AR160637	AR160637 Sequence
3	62	10.4	142373	2	AC122149	AC122149 Oryza sat
4	23	3.8	150347	2	AC027038	AC027038 Oryza sat
5	20	3.3	299350	1	SME591786	AL591786 Sinorhizo
6	19	3.2	1513	8	AY051059	AY051059 Arabidops
7	19	3.2	1867	8	AF370143	AF370143 Arabidops
c 8	19	3.2	4933	1	ABIPDC	X99587 A.brasilens
9	19	3.2	11470	1	AE012332	AE012332 Xanthomon
c 10	19	3.2	11570	1	AE003937	AE003937 Xylella f
11	19	3.2	82594	8	AC005311	AC005311 Arabidops
c 12	19	3.2	84872	8	AC006593	AC006593 Arabidops
13	19	3.2	346547	1	AP003012	AP003012 Mesorhizo
14	18	3.0	12325	1	AE001076	AE001076 Archaeogl
15	17	2.8	11368	1	AE011872	AE011872 Xanthomon
16	15	2.5	1124	3	PFA10B	J03986 P.falciparu

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 14, 2003, 02:29:20 ; Search time 337 Seconds  
(without alignments)  
4002.810 Million cell updates/sec

Title: US-09-846-589A-10  
Perfect score: 599  
Sequence: 1 TLPCLLSTTPLSPPPPPQI.....MDEPSGTVWRPCEPERSEES 599

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4368727

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

-  
Q=/cgn2\_1/USPTO\_spool/US09846589/runat\_13012003\_094910\_7714/app\_query.fasta\_1.77  
5

-DB=N\_Geneseq\_101002 -QFMT=fastap -SUFFIX=olip2n.rng -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=quality -THR\_MIN=1 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09846589\_@CGN\_1\_1\_0\_@runat\_13012003\_094910\_7714 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_101002:\*  
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:\*  
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:\*  
3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:\*  
4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:\*  
5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:\*  
6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:\*  
7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:\*  
8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:\*  
9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:\*  
10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:\*  
11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:\*

12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:\*  
 13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:\*  
 14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:\*  
 15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:\*  
 16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:\*  
 17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:\*  
 18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:\*  
 19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:\*  
 20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:\*  
 21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:\*  
 22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:\*  
 23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:\*  
 24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	599	100.0	2085	22	AAD07973			Corn cysteinyl-tRN
	2	76	12.7	1957	22	AAD07974			Rice cysteinyl-tRN
	3	41	6.8	294	24	ABL72570			Corn tassel-derive
	4	15	2.5	1142	21	AAC41815			Arabidopsis thalia
	5	14	2.3	2183	22	AAD07975			Soybean cysteinyl-
	6	14	2.3	10620	23	ABL17327			Drosophila melanog
	7	14	2.3	12748	23	ABL17326			Drosophila melanog
c	8	13	2.2	949	12	AAQ10542			E.coli peptidyl-pr
c	9	13	2.2	949	16	AAQ86973			Clone contg. E. co
c	10	13	2.2	949	16	AAQ86966			Clone contg. E. co
	11	13	2.2	92407	22	AAF28549			Genomic fragment #
c	12	13	2.2	92934	21	AAA81473			N. meningitidis pa
c	13	13	2.2	172325	21	AAF21613			Neisseria meningit
	14	13	2.2	349980	22	AAH41226			Pyrococcus abyssi
c	15	13	2.2	837096	21	AAA81489			N. meningitidis pa
	16	12	2.0	749	24	ABK78323			Bacillus clausii g
	17	12	2.0	1117	21	AAC97316			Helicobacter pylor
	18	12	2.0	1398	18	AAV25143			H. pylori cytoplas
	19	12	2.0	1399	24	ABK73872			Bacillus lichenifo
	20	12	2.0	2068	21	AAC77671			Human cancer assoc
	21	12	2.0	2426	23	ABL10423			Drosophila melanog
	22	12	2.0	2535	22	AAS45013			cDNA encoding nove
	23	12	2.0	2536	21	AAZ51261			Human RNA-associat
	24	12	2.0	2540	24	ABK51340			cDNA encoding huma
	25	12	2.0	2555	22	AAS45201			cDNA encoding nove
	26	12	2.0	2711	23	ABV22217			Human prostate exp
	27	12	2.0	4353	23	AAS75024			DNA encoding novel
	28	12	2.0	4381	23	AAS92743			DNA encoding novel
c	29	12	2.0	4733	23	ABL10422			Drosophila melanog
	30	12	2.0	19407	22	ABA15879			Human nervous syst
	31	12	2.0	19407	22	AAK81438			Human immune/haema
	32	11	1.8	1212	22	AAH66635			C glutamicum codin
	33	11	1.8	1416	24	ABQ68090			Listeria monocytog
	34	11	1.8	1605	24	ABQ69120			Listeria monocytog

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 14, 2003, 04:51:01 ; Search time 294 Seconds  
(without alignments)  
896.673 Million cell updates/sec

Title: US-09-846-589A-10  
Perfect score: 599  
Sequence: 1 TLPCLLSTTPLSPPPPPQI.....MDEPSGTVWRPCEPERSEES 599

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 389086 seqs, 220051671 residues

Word size: 1

Total number of hits satisfying chosen parameters: 777091

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

-

Q=/cgn2\_1/USPTO\_spool/US09846589/runat\_13012003\_094913\_7779/app\_query.fasta\_1.77  
5

-DB=Published\_Applications\_NA -QFMT=fastap -SUFFIX=olip2n.rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=quality -THR\_MIN=1  
-ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09846589 @CGN\_1\_1\_28 @runat\_13012003\_094913\_7779  
-NCPU=6 -ICPU=3 -NO\_XLPXY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_NA:\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*

12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	81	13.5	249	10	US-09-923-876-1857	Sequence 1857, Ap
2	41	6.8	294	10	US-09-294-093B-1944	Sequence 1944, Ap
3	12	2.0	366	10	US-09-960-352-2926	Sequence 2926, Ap
4	12	2.0	749	10	US-09-974-300-5614	Sequence 5614, Ap
5	12	2.0	1399	10	US-09-974-300-1163	Sequence 1163, Ap
6	12	2.0	2068	10	US-09-925-301-65	Sequence 65, Appl
7	11	1.8	1212	9	US-09-738-626-1670	Sequence 1670, Ap
c 8	11	1.8	640681	10	US-09-790-988-1	Sequence 1, Appli
c 9	11	1.8	3309400	9	US-09-738-626-1	Sequence 1, Appli
c 10	10	1.7	181	10	US-09-815-242-3450	Sequence 3450, Ap
11	10	1.7	671	10	US-09-764-853-106	Sequence 106, App
12	10	1.7	1399	10	US-09-815-242-4732	Sequence 4732, Ap
c 13	10	1.7	10636	10	US-09-070-927A-74	Sequence 74, Appl
14	10	1.7	11950	10	US-09-764-853-899	Sequence 899, App
c 15	9	1.5	100	10	US-09-969-373-1505	Sequence 1505, Ap
16	9	1.5	248	10	US-09-960-352-277	Sequence 277, App
17	9	1.5	463	10	US-09-864-761-5509	Sequence 5509, Ap
c 18	9	1.5	479	10	US-09-864-761-768	Sequence 768, App
19	9	1.5	489	10	US-09-244-694-153	Sequence 153, App
20	9	1.5	496	9	US-09-728-444-245	Sequence 245, App
21	9	1.5	531	10	US-09-864-761-22281	Sequence 22281, A
22	9	1.5	560	10	US-09-728-446-940	Sequence 940, App
c 23	9	1.5	581	10	US-09-822-849A-31	Sequence 31, Appl
c 24	9	1.5	830	10	US-09-864-761-19531	Sequence 19531, A
25	9	1.5	1380	9	US-09-738-626-2903	Sequence 2903, Ap
c 26	9	1.5	15295	10	US-09-764-877-3404	Sequence 3404, Ap
27	9	1.5	42999	9	US-09-799-462A-17	Sequence 17, Appl
28	9	1.5	42999	9	US-10-125-767-17	Sequence 17, Appl
c 29	9	1.5	62944	10	US-09-954-456-2257	Sequence 2257, Ap
c 30	9	1.5	126512	10	US-09-804-474A-3	Sequence 3, Appli
31	8	1.3	96	10	US-09-969-373-1233	Sequence 1233, Ap
32	8	1.3	108	10	US-09-969-373-1232	Sequence 1232, Ap
33	8	1.3	154	10	US-09-770-696-461	Sequence 461, App
34	8	1.3	237	10	US-09-783-590-5502	Sequence 5502, Ap
35	8	1.3	256	10	US-09-764-878-337	Sequence 337, App
36	8	1.3	261	10	US-09-864-761-17114	Sequence 17114, A
37	8	1.3	284	10	US-09-783-590-3447	Sequence 3447, Ap
c 38	8	1.3	287	10	US-09-864-761-22823	Sequence 22823, A
39	8	1.3	299	10	US-09-864-761-23550	Sequence 23550, A
40	8	1.3	322	10	US-09-833-381-1444	Sequence 1444, Ap
c 41	8	1.3	341	10	US-09-920-300A-1410	Sequence 1410, Ap
c 42	8	1.3	341	12	US-10-033-528-1410	Sequence 1410, Ap
c 43	8	1.3	366	10	US-09-878-574-4418	Sequence 4418, Ap
c 44	8	1.3	373	10	US-09-864-761-11275	Sequence 11275, A

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 14, 2003, 03:46:08 ; Search time 2318 Seconds  
(without alignments)  
4185.115 Million cell updates/sec

Title: US-09-846-589A-10  
Perfect score: 599  
Sequence: 1 TLPCLLSTTPLSPPPPPQI.....MDEPSGTVWRPCEPERSEES 599

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Word size: 1

Total number of hits satisfying chosen parameters: 32308016

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool/US09846589/runat\_13012003\_094912\_7752/app\_query.fasta\_1.77  
5

-DB=EST -QFMT=fastap -SUFFIX=olip2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=quality -THR\_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto  
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09846589\_@CGN\_1\_1\_887\_@runat\_13012003\_094912\_7752 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*

12: gb\_est3:\*  
 13: gb\_est4:\*  
 14: gb\_est5:\*  
 15: em\_estfun:\*  
 16: em\_estom:\*  
 17: gb\_gss:\*  
 18: em\_gss\_hum:\*  
 19: em\_gss\_inv:\*  
 20: em\_gss\_pln:\*  
 21: em\_gss\_vrt:\*  
 22: em\_gss\_fun:\*  
 23: em\_gss\_mam:\*  
 24: em\_gss\_mus:\*  
 25: em\_gss\_other:\*  
 26: em\_gss\_pro:\*  
 27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	%					Description
	No.	Score	Query Match Length DB ID			
	1	599	100.0	2120	11	AY104190 Zea mays
	2	168	28.0	581	10	AW065368 614048G07
	3	161	26.9	548	13	BM498016 952021B05
	4	155	25.9	624	10	AW065367 614048G06
	5	146	24.4	522	13	BM428660 952021B05
	6	141	23.5	636	10	AW065483 614058H08
	7	135	22.5	451	13	BM498280 952021B05
	8	135	22.5	588	10	AW497943 660042A12
c	9	128	21.4	577	10	AW000193 614058H08
c	10	118	19.7	470	9	AI947463 614048G07
	11	118	19.7	478	14	BQ667879 946101G05
c	12	117	19.5	548	14	BQ667878 946101G05
	13	117	19.5	586	10	AW563004 660070H04
c	14	97	16.2	604	9	AI746204 605082F05
	15	94	15.7	393	14	BQ778947 946115G02
c	16	83	13.9	594	10	AW600543 660070H04
	17	73	12.2	508	9	AI649625 486068G03
c	18	66	11.0	504	10	AW498128 660042A12
	19	57	9.5	412	14	BQ282680 WHE3080_D
	20	57	9.5	547	10	BE593605 WS1_98_F1
c	21	55	9.2	327	9	AI939893 618026C01
	22	52	8.7	584	14	BQ294221 1091026H1
	23	51	8.5	535	12	BG411263 EM1_27_F0
	24	51	8.5	647	10	BE593197 WS1_98_F1
c	25	49	8.2	615	9	AI622640 486105A09
	26	47	7.8	609	10	AV833385 AV833385
	27	47	7.8	614	13	BM135900 WHE2619_H
	28	41	6.8	500	14	BQ839424 WHE4165_H
	29	41	6.8	502	10	BE497913 WHE0958_G
	30	41	6.8	598	10	BE499567 WHE0962_H
	31	41	6.8	653	14	BQ838563 WHE2912_A



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 14, 2003, 00:41:52 ; Search time 4459 Seconds  
(without alignments)  
3909.527 Million cell updates/sec

Title: US-09-846-589A-10  
Perfect score: 3138  
Sequence: 1 TLPCLLSTTPLSPPPPPQI.....MDEPSGTVWRPCEPERSEES 599

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

-  
Q=/cgn2\_1/USPTO\_spool/US09846589/runat\_13012003\_094837\_7387/app\_query.fasta\_1.77  
5

-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09846589\_@CGN\_1\_1\_1879\_@runat\_13012003\_094837\_7387 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*

*Seq Search Summary  
for Seq 10  
(amino acid against DNA  
databases)*

*Identity*

11: gb\_sts:\*  
 12: gb\_sy:\*  
 13: gb\_un:\*  
 14: gb\_vi:\*  
 15: em\_ba:\*  
 16: em\_fun:\*  
 17: em\_hum:\*  
 18: em\_in:\*  
 19: em\_mu:\*  
 20: em\_om:\*  
 21: em\_or:\*  
 22: em\_ov:\*  
 23: em\_pat:\*  
 24: em\_ph:\*  
 25: em\_pl:\*  
 26: em\_ro:\*  
 27: em\_sts:\*  
 28: em\_un:\*  
 29: em\_vi:\*  
 30: em\_htg\_hum:\*  
 31: em\_htg\_inv:\*  
 32: em\_htg\_other:\*  
 33: em\_htg\_mus:\*  
 34: em\_htg\_pln:\*  
 35: em\_htg\_rod:\*  
 36: em\_htg\_mam:\*  
 37: em\_htg\_vrt:\*  
 38: em\_sy:\*  
 39: em\_htgo\_hum:\*  
 40: em\_htgo\_mus:\*  
 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		Query					Description
No.	Score	Match	Length	DB	ID		
	1	3138	100.0	2085	6	AR160636	AR160636 Sequence
	2	2398	76.4	1957	6	AR160637	AR160637 Sequence
	3	1934.5	61.6	142373	2	AC122149	AC122149 Oryza sat
	4	1585.5	50.5	150347	2	AC027038	AC027038 Oryza sat
	5	1536	48.9	1867	8	AF370143	AF370143 Arabidops
	6	1517	48.3	1513	8	AY051059	AY051059 Arabidops
	7	1470	46.8	2183	6	AR160638	AR160638 Sequence
	8	1150	36.6	82594	8	AC005311	AC005311 Arabidops
c	9	1150	36.6	84872	8	AC006593	AC006593 Arabidops
c	10	1142	36.4	71736	8	AB009048	AB009048 Arabidops
	11	1142	36.4	99492	8	ATF18021	AL163763 Arabidops
	12	1033.5	32.9	11615	1	AE010214	AE010214 Pyrococcu
	13	1014	32.3	10020	1	AE005233	AE005233 Escherich
	14	1014	32.3	262278	1	AP002552	AP002552 Escherich
c	15	1013	32.3	233000	1	AP000003	AP000003 Pyrococcu
c	16	1012	32.2	10461	1	U32693	U32693 Haemophilus

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 13, 2003, 22:31:52 ; Search time 337 Seconds  
(without alignments)  
4002.810 Million cell updates/sec

Title: US-09-846-589A-10  
Perfect score: 3138  
Sequence: 1 TLPCLLSTTPLSPPPPPQI.....MDEPSGTVWRPCEPERSEES 599

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool/US09846589/runat\_13012003\_094836\_7369/app\_query.fasta\_1.77  
5

-DB=N\_Geneseq\_101002 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09846589\_@CGN\_1\_1\_0\_@runat\_13012003\_094836\_7369 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_101002:\*

1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*  
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*  
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*  
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*  
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*  
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*  
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*  
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*  
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*  
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*  
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*

12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:\*  
 13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:\*  
 14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:\*  
 15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:\*  
 16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:\*  
 17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:\*  
 18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:\*  
 19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:\*  
 20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:\*  
 21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:\*  
 22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:\*  
 23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:\*  
 24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result			%				
No.	Score	Match	Query	Length	DB	ID	Description
	1	3138	100.0	2085	22	AAD07973	Corn cysteinyl-tRN
	2	2398	76.4	1957	22	AAD07974	Rice cysteinyl-tRN
	3	1470	46.8	2183	22	AAD07975	Soybean cysteinyl-
	4	1004	32.0	92407	22	AAF28549	Genomic fragment #
	5	987.5	31.5	1399	24	ABK73872	Bacillus lichenifo
	6	983	31.3	349980	22	AAH41226	Pyrococcus abyssi
c	7	975	31.1	92934	21	AAA81473	N. meningitidis pa
c	8	975	31.1	172325	21	AAF21613	Neisseria meningit
c	9	975	31.1	837096	21	AAA81489	N. meningitidis pa
c	10	911	29.0	10636	20	AAH13011	Enterococcus faeca
	11	901.5	28.7	3011208	24	ABQ69245	Listeria innocua D
	12	888.5	28.3	1416	24	ABQ68090	Listeria monocytog
	13	888.5	28.3	1163020	24	ABQ67197	Listeria innocua c
	14	887.5	28.3	2944528	24	ABA03041	Listeria monocytog
	15	879.5	28.0	1440	24	ABN91828	Staphylococcus epi
c	16	879.5	28.0	3242	22	AAH54369	S. epidermidis gen
c	17	873	27.8	640681	24	ABA92787	Buchnera sp. genom
	18	869	27.7	1344	18	AAT97093	Streptococcus pneu
c	19	863	27.5	28882	19	AAV52273	Streptococcus pneu
	20	862.5	27.5	1401	18	AAT72875	DNA encoding cyste
	21	862.5	27.5	1401	19	AAV31108	Staphylococcus aur
	22	862.5	27.5	1401	21	AAA39270	Staphylococcus aur
	23	854.5	27.2	1399	23	AAS52150	Staphylococcus aur
	24	851	27.1	1341	24	ABN66316	Streptococcus poly
	25	851	27.1	2155561	24	ABN71527	Streptococcus poly
c	26	831	26.5	2365589	24	ABA90521	Genomic sequence o
	27	830	26.4	1341	24	ABN66317	Streptococcus poly
	28	793	25.3	2633	24	ABQ70829	Listeria monocytog
	29	779	24.8	1380	22	AAH67868	C glutamicum codin
c	30	779	24.8	349980	22	AAH68533	C glutamicum codin
	31	774	24.7	1398	18	AAV25143	H. pylori cytoplas
c	32	773	24.6	13336	23	AAS59554	Propionibacterium
	33	770	24.5	1142	21	AAC41815	Arabidopsis thalia
c	34	748.5	23.9	6876	18	AAV74497	Staphylococcus aur

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 13, 2003, 23:14:27 ; Search time 66 Seconds  
(without alignments)  
2783.324 Million cell updates/sec

Title: US-09-846-589A-10  
Perfect score: 3138  
Sequence: 1 TLPCLLSTTPLSPPPPPQI.....MDEPSGTVWRPCEPERSEES 599

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool/US09846589/runat\_13012003\_094836\_7377/app\_query.fasta\_1.77  
5

-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09846589\_@CGN\_1\_1\_19\_@runat\_13012003\_094836\_7377 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MMMap -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3138	100.0	2085	4	US-09-352-990-9	Sequence 9, Appli
2	2398	76.4	1957	4	US-09-352-990-11	Sequence 11, Appl
3	1470	46.8	2183	4	US-09-352-990-13	Sequence 13, Appl
4	879.5	28.0	1440	4	US-09-134-001C-1291	Sequence 1291, Ap
5	869	27.7	1344	1	US-08-844-010-1	Sequence 1, Appli
6	869	27.7	1344	3	US-09-012-873-1	Sequence 1, Appli
c 7	863	27.5	28882	4	US-08-961-527-140	Sequence 140, App
8	862.5	27.5	1401	1	US-08-785-066-1	Sequence 1, Appli
9	862.5	27.5	1401	3	US-09-007-355-1	Sequence 1, Appli
10	862.5	27.5	1401	3	US-08-913-489-1	Sequence 1, Appli
c 11	745.5	23.8	4403765	4	US-09-103-840A-2	Sequence 2, Appli
c 12	745.5	23.8	4411529	4	US-09-103-840A-1	Sequence 1, Appli
13	722.5	23.0	1494	3	US-08-898-977-1	Sequence 1, Appli
14	722.5	23.0	1494	4	US-09-535-171-1	Sequence 1, Appli
c 15	504	16.1	1360	4	US-08-858-207A-65	Sequence 65, Appl
16	458	14.6	2083	4	US-09-221-017B-938	Sequence 938, App
17	363.5	11.6	333	1	US-08-844-010-3	Sequence 3, Appli
18	363.5	11.6	333	3	US-09-012-873-3	Sequence 3, Appli
19	162.5	5.2	1983	4	US-09-134-001C-513	Sequence 513, App
c 20	148.5	4.7	10690	4	US-08-961-527-93	Sequence 93, Appl
21	148	4.7	5163	3	US-08-700-651-1	Sequence 1, Appli
22	148	4.7	5163	3	US-08-928-361B-4	Sequence 4, Appli
23	148	4.7	5318	3	US-08-700-651-2	Sequence 2, Appli
24	148	4.7	5318	3	US-08-928-361B-3	Sequence 3, Appli
25	146.5	4.7	1998	3	US-08-844-059-1	Sequence 1, Appli
26	146.5	4.7	1998	4	US-09-431-202-1	Sequence 1, Appli
27	144.5	4.6	1897	1	US-08-453-477-1	Sequence 1, Appli
28	144.5	4.6	1897	1	US-08-453-461-1	Sequence 1, Appli
29	144	4.6	5661	4	US-08-938-105-2	Sequence 2, Appli
30	137.5	4.4	3574	4	US-09-311-236-1	Sequence 1, Appli
31	136.5	4.3	4945	4	US-08-961-527-47	Sequence 47, Appl
32	134.5	4.3	4911	4	US-09-718-692-1	Sequence 1, Appli
33	134.5	4.3	4911	4	US-09-718-852-1	Sequence 1, Appli
34	134.5	4.3	4911	4	US-09-718-815-1	Sequence 1, Appli
35	130	4.1	397	3	US-09-253-691-3	Sequence 3, Appli
36	128	4.1	954	4	US-08-098-327E-37	Sequence 37, Appl
37	128	4.1	954	4	US-08-462-625-37	Sequence 37, Appl
38	128	4.1	988	4	US-08-098-327E-34	Sequence 34, Appl
39	128	4.1	988	4	US-08-462-625-34	Sequence 34, Appl
40	126	4.0	2085	2	US-08-668-128B-7	Sequence 7, Appli
41	126	4.0	2085	2	US-08-905-445-7	Sequence 7, Appli
42	123	3.9	3279	4	US-08-446-137B-1	Sequence 1, Appli
43	123	3.9	6921	4	US-09-643-597-117	Sequence 117, App
44	122.5	3.9	1784	6	5180810-2	Patent No. 5180810
45	122	3.9	950	4	US-08-098-327E-32	Sequence 32, Appl

## ALIGNMENTS

RESULT 1

US-09-352-990-9

; Sequence 9, Application US/09352990

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 14, 2003, 00:53:57 ; Search time 81 Seconds  
(without alignments)  
3254.591 Million cell updates/sec

Title: US-09-846-589A-10  
Perfect score: 3138  
Sequence: 1 TLPCLLSTTPLSPPPPPQI.....MDEPSGTVWRPCEPERSEES 599

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 389086 seqs, 220051671 residues

Total number of hits satisfying chosen parameters: 778172

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool/US09846589/runat\_13012003\_094839\_7435/app\_query.fasta\_1.77  
5

-DB=Published\_Applications\_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09846589\_@CGN\_1\_1\_28\_@runat\_13012003\_094839\_7435  
-NCPU=6 -ICPU=3 -NO\_XLPXY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_NA:\*  
1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*

12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	%						Description
	No.	Score	Query Match	Length	DB	ID	
	1	987.5	31.5	1399	10	US-09-974-300-1163	Sequence 1163, Ap
c	2	911	29.0	10636	10	US-09-070-927A-74	Sequence 74, Appl
c	3	873	27.8	640681	10	US-09-790-988-1	Sequence 1, Appli
	4	854.5	27.2	1399	10	US-09-815-242-4732	Sequence 4732, Ap
	5	779	24.8	1380	9	US-09-738-626-2903	Sequence 2903, Ap
c	6	779	24.8	3309400	9	US-09-738-626-1	Sequence 1, Appli
	7	644	20.5	2068	10	US-09-925-301-65	Sequence 65, Appl
	8	622	19.8	1212	9	US-09-738-626-1670	Sequence 1670, Ap
	9	453.5	14.5	749	10	US-09-974-300-5614	Sequence 5614, Ap
	10	406	12.9	249	10	US-09-923-876-1857	Sequence 1857, Ap
	11	321	10.2	294	10	US-09-294-093B-1944	Sequence 1944, Ap
	12	256.5	8.2	366	10	US-09-960-352-2926	Sequence 2926, Ap
	13	248.5	7.9	727	9	US-09-895-913A-77	Sequence 77, Appl
c	14	247	7.9	181	10	US-09-815-242-3450	Sequence 3450, Ap
	15	151	4.8	1974	10	US-09-815-242-8037	Sequence 8037, Ap
	16	150.5	4.8	1626	10	US-09-815-242-7219	Sequence 7219, Ap
	17	150.5	4.8	2040	10	US-09-815-242-9320	Sequence 9320, Ap
	18	147	4.7	1998	10	US-09-815-242-3878	Sequence 3878, Ap
	19	147	4.7	2034	10	US-09-815-242-6566	Sequence 6566, Ap
	20	147	4.7	9589	10	US-09-070-927A-256	Sequence 256, App
	21	145	4.6	1974	10	US-09-815-242-8915	Sequence 8915, Ap
	22	137.5	4.4	3574	10	US-09-912-917-1	Sequence 1, Appli
	23	135	4.3	1960	10	US-09-815-242-4841	Sequence 4841, Ap
	24	134	4.3	4937	12	US-10-044-090-76	Sequence 76, Appl
	25	130.5	4.2	8493	9	US-10-071-766-51	Sequence 51, Appl
	26	129.5	4.1	4286	9	US-09-849-243-14	Sequence 14, Appl
	27	129.5	4.1	4519	9	US-10-108-605-132	Sequence 132, App
	28	128.5	4.1	5607	9	US-10-108-605-92	Sequence 92, Appl
	29	128	4.1	954	10	US-09-837-344-37	Sequence 37, Appl
	30	128	4.1	988	10	US-09-837-344-34	Sequence 34, Appl
	31	127	4.0	14800	10	US-09-954-456-1601	Sequence 1601, Ap
	32	126.5	4.0	1518	10	US-09-815-242-7220	Sequence 7220, Ap
	33	126.5	4.0	2850	9	US-09-954-531-388	Sequence 388, App
	34	126.5	4.0	4916	10	US-09-866-108-5	Sequence 5, Appli
	35	126.5	4.0	7707	10	US-09-866-108-2	Sequence 2, Appli
	36	126.5	4.0	8117	10	US-09-866-108-1	Sequence 1, Appli
	37	126	4.0	1791	10	US-09-416-384A-6	Sequence 6, Appli
	38	126	4.0	4001	9	US-10-098-841-39	Sequence 39, Appl
	39	126	4.0	6604	10	US-09-880-107-1748	Sequence 1748, Ap
	40	125	4.0	1310	9	US-09-849-243-13	Sequence 13, Appl
	41	125	4.0	3263	9	US-09-849-243-15	Sequence 15, Appl
	42	125	4.0	6386	9	US-10-098-841-40	Sequence 40, Appl
	43	125	4.0	7497	10	US-09-960-253-175	Sequence 175, App
	44	125	4.0	7792	12	US-10-044-090-359	Sequence 359, App



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 14, 2003, 00:50:47 ; Search time 2287 Seconds  
(without alignments)  
4241.844 Million cell updates/sec

Title: US-09-846-589A-10  
Perfect score: 3138  
Sequence: 1 TLPCLLSTTPLSPPPPPQI.....MDEPSGTVWRPCEPERSEES 599

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

-

Q=/cgn2\_1/USPTO\_spool/US09846589/runat\_13012003\_094838\_7402/app\_query.fasta\_1.77  
5

-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09846589\_CGN\_1\_1\_887\_runat\_13012003\_094838\_7402 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*

12: gb\_est3:\*  
 13: gb\_est4:\*  
 14: gb\_est5:\*  
 15: em\_estfun:\*  
 16: em\_estom:\*  
 17: gb\_gss:\*  
 18: em\_gss\_hum:\*  
 19: em\_gss\_inv:\*  
 20: em\_gss\_pln:\*  
 21: em\_gss\_vrt:\*  
 22: em\_gss\_fun:\*  
 23: em\_gss\_mam:\*  
 24: em\_gss\_mus:\*  
 25: em\_gss\_other:\*  
 26: em\_gss\_pro:\*  
 27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	3138	100.0	2120	11	AY104190	AY104190 Zea mays
2	997	31.8	652	14	BQ465217	BQ465217 HU02P15r
3	960	30.6	609	10	AV833385	AV833385 AV833385
4	956.5	30.5	588	10	AW497943	AW497943 660042A12
5	952	30.3	548	13	BM498016	BM498016 952021B05
6	920	29.3	614	13	BM135900	BM135900 WHE2619_H
7	919.5	29.3	643	13	BJ463548	BJ463548 BJ463548
8	900	28.7	581	10	AW065368	AW065368 614048G07
9	882	28.1	522	13	BM428660	BM428660 952021B05
10	820	26.1	535	12	BG411263	BG411263 EM1_27_F0
11	808	25.7	624	10	AW065367	AW065367 614048G06
12	793	25.3	693	9	AL507468	AL507468 AL507468
13	783	25.0	589	13	BJ245810	BJ245810 BJ245810
14	781	24.9	547	10	BE593605	BE593605 WS1_98_F1
15	778	24.8	1887	17	BH770866	BH770866 LLMGtag60
16	767	24.4	451	13	BM498280	BM498280 952021B05
17	763.5	24.3	595	14	BQ468212	BQ468212 HP01G15T
18	740	23.6	600	12	BG521662	BG521662 13-20 Ste
19	716	22.8	500	14	BQ839424	BQ839424 WHE4165_H
20	716	22.8	629	14	BQ490648	BQ490648 96-E01178
21	710	22.6	478	14	BQ667879	BQ667879 946101G05
22	708	22.6	611	12	BG451468	BG451468 NF110F10D
23	705.5	22.5	700	9	AL507494	AL507494 AL507494
24	698	22.2	636	10	AW065483	AW065483 614058H08
25	696.5	22.2	653	14	BQ838563	BQ838563 WHE2912_A
26	691	22.0	1798	11	AK009937	AK009937 Mus muscu
c 27	656.5	20.9	692	13	BJ466496	BJ466496 BJ466496
28	649.5	20.7	694	10	AW906351	AW906351 EST342473
29	647	20.6	658	12	BG448141	BG448141 NF106G06E
30	644	20.5	718	14	BQ860453	BQ860453 QGC15M18.
31	642	20.5	551	13	BM526332	BM526332 sal40a03.